

SEQUENCE LISTING

<110> Gurney, Mark E.

Li, Jinhe

Pauley, Adele M.

Pharmacia & Upjohn Company

<120> Human Sel-10 Polypeptides and Polynucleotides that Encode Them

<130> 6142

<140> 6142

<141> 1997-12-19

<160> 2/ 32

<170> PatentIn Ver. 2.0

D2

<210> 1

<211> 3550

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (2485)

<220>

<221> unsure

<222> (3372)

<400> 1

ctcattattc cctcgagttc ttctcagtca agctgcatgt atgtatgtgt gtcccgagaa 60 gcggtttgat actgagctgc atttgccttt actgtggagt tttgttgccg gttctgctcc 120 ctaatcttcc ttttctgacg tgcctgagca tgtccacatt agaatctgtg acatacctac 180 ctgaaaaagg tttatattgt cagagactgc caagcagccg gacacacggg ggcacagaat 240

RECEIVED
NAR 1 0 7003
TECH CENTER 1800/2900

cactgaaggg gaaaaataca gaaaatatgg gtttctacgg cacattaaaa atgatttttt 300 acaaaatgaa aagaaagttg gaccatggtt ctgaggtccg ctctttttct ttgggaaaga 360 aaccatgcaa agtotcagaa tatacaagta ccactgggot tgtaccatgt tcagcaacac 420 caacaacttt tggggacctc agagcagcca atggccaagg gcaacaacga cgccgaatta 480 catctgtcca gccacctaca ggcctccagg aatggctaaa aatgtttcag agctggagtg 540 gaccagagaa attgcttgct ttagatgaac tcattgatag ttgtgaacca acacaagtaa 600 aacatatgat gcaagtgata gaaccccagt ttcaacgaga cttcatttca ttgctcccta 660 aagagttggc actctatgtg ctttcattcc tggaacccaa agacctgcta caagcagctc 720 agacatgtcg ctactggaga attttggctg aagacaacct tctctggaga gagaaatgca 780 aagaagaggg gattgatgaa ccattgcaca tcaagagaag aaaagtaata aaaccaggtt 840 tcatacacag tccatggaaa agtgcataca tcagacagca cagaattgat actaactgga 900 ggcgaggaga actcaaatct cctaaggtgc tgaaaggaca tgatgatcat gtgatcacat 960 gcttacagtt ttgtggtaac cgaatagtta gtggttctga tgacaacact ttaaaagttt 1020 ggtcagcagt cacaggcaaa tgtctgagaa cattagtggg acatacaggt ggagtatggt 1080 catcacaaat gagagacaac atcatcatta gtggatctac agatcggaca ctcaaagtgt 1140 ggaatgcaga gactggagaa tgtatacaca ccttatatgg gcatacttcc actgtgcgtt 1200 qtatqcatct tcatgaaaaa agagttgtta gcggttctcg agatgccact cttagggttt 1260 gggatattga gacaggccag tgtttacatg ttttgatggg tcatgttgca gcagtccgct 1320 gtgttcaata tgatggcagg agggttgtta gtggagcata tgattttatg gtaaaggtgt 1380 gggatccaga gactgaaacc tgtctacaca cgttgcaggg gcatactaat agagtctatt 1440 cattacagtt tgatggtatc catgtggtga gtggatctct tgatacatca atccgtgttt 1500 gggatgtgga gacagggaat tgcattcaca cgttaacagg gcaccagtcg ttaacaagtg 1560 gaatggaact caaagacaat attettgtet etgggaatge agattetaca gttaaaatet 1620 gggatatcaa aacaggacag tgtttacaaa cattgcaagg tcccaacaag catcagagtg 1680 ctgtgacctg tttacagttc aacaagaact ttgtaattac cagctcagat gatggaactg 1740 taaaactatg ggacttgaaa acgggtgaat ttattcgaaa cctagtcaca ttggagagtg 1800 gggggagtgg gggagttgtg tggcggatca gagcctcaaa cacaaagctg gtgtgtgcag 1860 ttgggagtcg gaatgggact gaagaaacca agctgctggt gctggacttt gatgtggaca 1920 tgaagtgaag agcagaaaag atgaatttgt ccaattgtgt agacgatata ctccctgccc 1980 ttccccctgc aaaaagaaaa aaagaaaaga aaaagaaaaa aatcccttgt tctcagtggt 2040 gcaggatgtt ggcttggggc aacagattga aaagacctac agactaagaa ggaaaagaag 2100 aagagatgac aaaccataac tgacaagaga ggcgtctgct gtctcatcac ataaaaggct 2160 tcacttttga ctgagggcag ctttgcaaaa tgagactttc taaatcaaac caggtgcaat 2220 tatttettta ttttettete eagtggteat tggggeagtg ttaatgetga aacateatta 2280





cagattetge tageetgtte ttttaceact gaeagetaga caeetagaaa ggaaetgeaa 2340 taatatcaaa acaagtactg gttgactttc taattagaga gcatctgcaa caaaaagtca 2400 tttttctgga gtggaaaagc ttaaaaaaaat tactgtgaat tgtttttgta cagttatcat 2460 gaaaagettt ttttttatt ttttngccaa ccattgccaa tgtcaatcaa tcacagtatt 2520 agcctctgtt aatctattta ctgttgcttc catatacatt cttcaatgca tatgttgctc 2580 aaaggtggca agttgtcctg ggttctgtga gtcctgagat ggatttaatt cttgatgctg 2640 gtgctagaag taggtcttca aatatgggat tgttgtccca accctgtact gtactcccag 2700 tggccaaact tatttatgct gctaaatgaa agaaagaaaa aagcaaatta tttttttat 2760 tttttttctg ctgtgacgtt ttagtcccag actgaattcc aaatttgctc tagtttggtt 2820 atggaaaaaa gactttttgc cactgaaact tgagccatct gtgcctctaa gaggctgaga 2880 atggaagagt ttcagataat aaagagtgaa gtttgcctgc aagtaaagaa ttgagagtgt 2940 gtgcaaagct tattttcttt tatctgggca aaaattaaaa cacattcctt ggaacagagc 3000 tattacttgc ctgttctgtg gagaaacttt tctttttgag ggctgtggtg aatggatgaa 3060 cgtacatcgt aaaactgaca aaatatttta aaaatatata aaacacaaaa ttaaaataaa 3120 gttgctggtc agtcttagtg ttttacagta tttgggaaaa caactgttac agttttattg 3180 ctctgagtaa ctgacaaagc agaaactatt cagtttttgt agtaaaggcg tcacatgcaa 3240 acaaacaaaa tgaatgaaac agtcaaatgg tttgcctcat tctccaagag ccacaactca 3300 agctgaactg tgaaagtggt ttaacactgt atcctaggcg atcttttttc ctccttctgt 3360 ttattttttt gnttgtttta tttatagtct gatttaaaac aatcagattc aagttggtta 3420 attttagtta tgtaacaacc tgacatgatg gaggaaaaca acctttaaag ggattgtgtc 3480 tatggtttga ttcacttaga aattttattt tcttataact taagtgcaat aaaatgtgtt 3540 3550 ttttcatgtt

D2

43

<210> 2

<211> 3571

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (2506)

<220>

<221> unsure

<222> (3393)

<400> 2

4

ctcagcaggt caggacattt ggtaggggaa ggttgaaaga caaaagcagc aggccttggg 60 ttctcagcct tttaaaaact attattaaat atatatttt aaaatttagt ggttagagct 120 tttagtaatg tgcctgtatt acatgtagag agtattcgtc aaccaagagg agttttaaaa 180 tgtcaaaacc gggaaaacct actctaaacc atggcttggt tcctgttgat cttaaaagtg 240 caaaagagcc tctaccacat caaaccgtga tgaagatatt tagcattagc atcattgccc 300 aaggeeteee tttttgtega agaeggatga aaagaaagtt ggaeeatggt tetgaggtee 360 gctctttttc tttgggaaag aaaccatgca aagtctcaga atatacaagt accactgggc 420 ttgtaccatg ttcagcaaca ccaacaactt ttggggacct cagagcagcc aatggccaag 480 ggcaacaacg acgccgaatt acatctgtcc agccacctac aggcctccag gaatggctaa 540 aaatgtttca gagctggagt ggaccagaga aattgcttgc tttagatgaa ctcattgata 600 gttgtgaacc aacacaagta aaacatatga tgcaagtgat agaaccccag tttcaacgag 660 acttcatttc attgctccct aaagagttgg cactctatgt gctttcattc ctggaaccca 720 aagacctgct acaagcagct cagacatgtc gctactggag aattttggct gaagacaacc 780 ttctctggag agagaaatgc aaagaagagg ggattgatga accattgcac atcaagagaa 840 gaaaagtaat aaaaccaggt ttcatacaca gtccatggaa aagtgcatac atcagacagc 900 acagaattga tactaactgg aggcgaggag aactcaaatc tcctaaggtg ctgaaaggac 960 atgatgatca tgtgatcaca tgcttacagt tttgtggtaa ccgaatagtt agtggttctg 1020 atgacaacac tttaaaagtt tggtcagcag tcacaggcaa atgtctgaga acattagtgg 1080 gacatacagg tggagtatgg tcatcacaaa tgagagacaa catcatcatt agtggatcta 1140 cagatcggac actcaaagtg tggaatgcag agactggaga atgtatacac accttatatg 1200 ggcatacttc cactgtgcgt tgtatgcatc ttcatgaaaa aagagttgtt agcggttctc 1260 gagatgccac tettagggtt tgggatattg agacaggeca gtgtttacat gttttgatgg 1320 gtcatgttgc agcagtccgc tgtgttcaat atgatggcag gagggttgtt agtggagcat 1380 atgattttat ggtaaaggtg tgggatccag agactgaaac ctgtctacac acgttgcagg 1440 ggcatactaa tagagtctat tcattacagt ttgatggtat ccatgtggtg agtggatctc 1500 ttgatacatc aatccgtgtt tgggatgtgg agacagggaa ttgcattcac acgttaacag 1560 ggcaccagtc gttaacaagt ggaatggaac tcaaagacaa tattcttgtc tctgggaatg 1620 cagattctac agttaaaatc tgggatatca aaacaggaca gtgtttacaa acattgcaag 1680 gtcccaacaa gcatcagagt gctgtgacct gtttacagtt caacaagaac tttgtaatta 1740 ccagctcaga tgatggaact gtaaaactat gggacttgaa aacgggtgaa tttattcgaa 1800 acctagtcac attggagagt ggggggagtg ggggagttgt gtggcggatc agagcctcaa 1860 acacaaagct ggtgtgtgca gttgggagtc ggaatgggac tgaagaaacc aagctgctgg 1920 tgctggactt tgatgtggac atgaagtgaa gagcagaaaa gatgaatttg tccaattgtg 1980

DZ



aaatcccttg ttctcagtgg tgcaggatgt tggcttgggg caacagattg aaaagaccta 2100 cagactaaga aggaaaagaa gaagagatga caaaccataa ctgacaagag aggcgtctgc 2160 tgtctcatca cataaaaggc ttcacttttg actgagggca gctttgcaaa atgagacttt 2220 ctaaatcaaa ccaggtgcaa ttatttcttt attttcttct ccagtggtca ttggggcagt 2280 gttaatgctg aaacatcatt acagattctg ctagcctgtt cttttaccac tgacagctag 2340 acacctagaa aggaactgca ataatatcaa aacaagtact ggttgacttt ctaattagag 2400 agcatctgca acaaaaagtc atttttctgg agtggaaaag cttaaaaaaa ttactgtgaa 2460 ttgtttttgt acagttatca tgaaaagctt ttttttttat tttttngcca accattgcca 2520 atgtcaatca atcacagtat tagcctctgt taatctattt actgttgctt ccatatacat 2580 tetteaatge atatgttget caaaggtgge aagttgteet gggttetgtg agteetgaga 2640 tggatttaat tettgatget ggtgetagaa gtaggtette aaatatggga ttgttgteee 2700 aaccctgtac tgtactccca gtggccaaac ttatttatgc tgctaaatga aagaaagaaa 2760 aaaqcaaatt atttttttta ttttttttct gctgtgacgt tttagtccca gactgaattc 2820 caaatttgct ctagtttggt tatggaaaaa agactttttg ccactgaaac ttgagccatc 2880 tgtgcctcta agaggctgag aatggaagag tttcagataa taaagagtga agtttgcctg 2940 caagtaaaga attgagagtg tgtgcaaagc ttattttctt ttatctgggc aaaaattaaa 3000 acacattect tggaacagag ctattacttg cetgttetgt ggagaaactt ttetttttga 3060 gggctgtggt gaatggatga acgtacatcg taaaactgac aaaatatttt aaaaatatat 3120 aaaacacaaa attaaaataa agttgctggt cagtcttagt gttttacagt atttgggaaa 3180 acaactgtta cagttttatt gctctgagta actgacaaag cagaaactat tcagtttttg 3240 tagtaaaggc gtcacatgca aacaaacaaa atgaatgaaa cagtcaaatg gtttgcctca 3300 ttotocaaga gocacaacto aagotgaact gtgaaagtgg tttaacactg tatoctaggc 3360 gatetttttt eeteettetg tttattttt tgnttgtttt atttatagte tgatttaaaa 3420 caatcagatt caagttggtt aattttagtt atgtaacaac ctgacatgat ggaggaaaac 3480 aacctttaaa gggattgtgt ctatggtttg attcacttag aaattttatt ttcttataac 3540 3571 ttaagtgcaa taaaatgtgt tttttcatgt t

12

<210> 3

<211> 627

<212> PRT

<213> Homo sapiens

<400> 3

Met Cys Val Pro Arg Ser Gly Leu Ile Leu Ser Cys Ile Cys Leu Tyr

1 5 10 15

á.

Cys Gly Val Leu Leu Pro Val Leu Leu Pro Asn Leu Pro Phe Leu Thr

Cys Leu Ser Met Ser Thr Leu Glu Ser Val Thr Tyr Leu Pro Glu Lys

35 40 45

Gly Leu Tyr Cys Gln Arg Leu Pro Ser Ser Arg Thr His Gly Gly Thr
50 55 60

Glu Ser Leu Lys Gly Lys Asn Thr Glu Asn Met Gly Phe Tyr Gly Thr
65 70 75 80

Leu Lys Met Ile Phe Tyr Lys Met Lys Arg Lys Leu Asp His Gly Ser

85 90 95

Glu Val Arg Ser Phe Ser Leu Gly Lys Lys Pro Cys Lys Val Ser Glu
100 105 110

Tyr Thr Ser Thr Thr Gly Leu Val Pro Cys Ser Ala Thr Pro Thr Thr

115 120 125

Phe Gly Asp Leu Arg Ala Ala Asn Gly Gln Gly Gln Gln Arg Arg Arg 130 135 140

Phe Gln Ser Trp Ser Gly Pro Glu Lys Leu Leu Ala Leu Asp Glu Leu 165 170 175

Ile Asp Ser Cys Glu Pro Thr Gln Val Lys His Met Met Gln Val Ile

180 185 190

4-

à.

Glu Pro Gln Phe Gln Arg Asp Phe Ile Ser Leu Leu Pro Lys Glu Leu 195 200 205

Ala Leu Tyr Val Leu Ser Phe Leu Glu Pro Lys Asp Leu Leu Gln Ala 210 215 220

Ala Gln Thr Cys Arg Tyr Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu 225 230 235 240

Trp Arg Glu Lys Cys Lys Glu Glu Gly Ile Asp Glu Pro Leu His Ile
245 250 255

Lys Arg Arg Lys Val Ile Lys Pro Gly Phe Ile His Ser Pro Trp Lys
260 265 270

Ser Ala Tyr Ile Arg Gln His Arg Ile Asp Thr Asn Trp Arg Arg Gly
275 280 285

Glu Leu Lys Ser Pro Lys Val Leu Lys Gly His Asp Asp His Val Ile 290 295 300

Thr Cys Leu Gln Phe Cys Gly Asn Arg Ile Val Ser Gly Ser Asp Asp 305 310 315 320

Asn Thr Leu Lys Val Trp Ser Ala Val Thr Gly Lys Cys Leu Arg Thr 325 330 335

Leu Val Gly His Thr Gly Gly Val Trp Ser Ser Gln Met Arg Asp Asn 340 345 350

Ile Ile Ile Ser Gly Ser Thr Asp Arg Thr Leu Lys Val Trp Asn Ala 355 360 365 Glu Thr Gly Glu Cys Ile His Thr Leu Tyr Gly His Thr Ser Thr Val 370 375 380

Arg Cys Met His Leu His Glu Lys Arg Val Val Ser Gly Ser Arg Asp 385 390 395 400

Ala Thr Leu Arg Val Trp Asp Ile Glu Thr Gly Gln Cys Leu His Val
405 410 415

Leu Met Gly His Val Ala Ala Val Arg Cys Val Gln Tyr Asp Gly Arg
420 425 430

Arg Val Val Ser Gly Ala Tyr Asp Phe Met Val Lys Val Trp Asp Pro 435 440 445

Glu Thr Glu Thr Cys Leu His Thr Leu Gln Gly His Thr Asn Arg Val
450 455 460

Tyr Ser Leu Gln Phe Asp Gly Ile His Val Val Ser Gly Ser Leu Asp
465 470 475 480

Thr Ser Ile Arg Val Trp Asp Val Glu Thr Gly Asn Cys Ile His Thr
485 490 495

Leu Thr Gly His Gln Ser Leu Thr Ser Gly Met Glu Leu Lys Asp Asn 500 505 510

Ile Leu Val Ser Gly Asn Ala Asp Ser Thr Val Lys Ile Trp Asp Ile
515 520 525

Lys Thr Gly Gln Cys Leu Gln Thr Leu Gln Gly Pro Asn Lys His Gln 530 535 540

Ser Ala Val Thr Cys Leu Gln Phe Asn Lys Asn Phe Val Ile Thr Ser 545 550 555 560

Ser Asp Asp Gly Thr Val Lys Leu Trp Asp Leu Lys Thr Gly Glu Phe 565 570 575

Ile Arg Asn Leu Val Thr Leu Glu Ser Gly Gly Ser Gly Gly Val Val
580 585 590

Trp Arg Ile Arg Ala Ser Asn Thr Lys Leu Val Cys Ala Val Gly Ser
595 600 605

Arg Asn Gly Thr Glu Glu Thr Lys Leu Leu Val Leu Asp Phe Asp Val 610 615 620

Asp Met Lys

625

ű.

<210> 4

<211> 592

<212> PRT

<213> Homo sapiens

<400> 4

Met Ser Thr Leu Glu Ser Val Thr Tyr Leu Pro Glu Lys Gly Leu Tyr

1 5 10 15

Cys Gln Arg Leu Pro Ser Ser Arg Thr His Gly Gly Thr Glu Ser Leu 20 25 30

Lys Gly Lys Asn Thr Glu Asn Met Gly Phe Tyr Gly Thr Leu Lys Met 35

Ile Phe Tyr Lys Met Lys Arg Lys Leu Asp His Gly Ser Glu Val Arg

Ser Phe Ser Leu Gly Lys Lys Pro Cys Lys Val Ser Glu Tyr Thr Ser

65 70 75 80

Thr Thr Gly Leu Val Pro Cys Ser Ala Thr Pro Thr Thr Phe Gly Asp

85 90 95

Leu Arg Ala Ala Asn Gly Gln Gly Gln Arg Arg Arg Ile Thr Ser
100 105 110

Val Gln Pro Pro Thr Gly Leu Gln Glu Trp Leu Lys Met Phe Gln Ser 115 120 125

Trp Ser Gly Pro Glu Lys Leu Leu Ala Leu Asp Glu Leu Ile Asp Ser 130 135 140

Cys Glu Pro Thr Gln Val Lys His Met Met Gln Val Ile Glu Pro Gln
145 150 155 160

Phe Gln Arg Asp Phe Ile Ser Leu Leu Pro Lys Glu Leu Ala Leu Tyr 165 170 175

Val Leu Ser Phe Leu Glu Pro Lys Asp Leu Leu Gln Ala Ala Gln Thr 180 185 190

Cys Arg Tyr Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu Trp Arg Glu
195 200 205

Lys Cys Lys Glu Glu Gly Ile Asp Glu Pro Leu His Ile Lys Arg Arg 210 215 220

Lys Val Ile Lys Pro Gly Phe Ile His Ser Pro Trp Lys Ser Ala Tyr

225 230 235 240

€.

Ile Arg Gln His Arg Ile Asp Thr Asn Trp Arg Arg Gly Glu Leu Lys
245 250 255

Ser Pro Lys Val Leu Lys Gly His Asp Asp His Val Ile Thr Cys Leu 260 265 270

Gln Phe Cys Gly Asn Arg Ile Val Ser Gly Ser Asp Asn Thr Leu 275 280 285

Lys Val Trp Ser Ala Val Thr Gly Lys Cys Leu Arg Thr Leu Val Gly
290 295 300

His Thr Gly Gly Val Trp Ser Ser Gln Met Arg Asp Asn Ile Ile Ile 305 310 315 320

Ser Gly Ser Thr Asp Arg Thr Leu Lys Val Trp Asn Ala Glu Thr Gly
325 330 335

Glu Cys Ile His Thr Leu Tyr Gly His Thr Ser Thr Val Arg Cys Met 340 345 350

His Leu His Glu Lys Arg Val Val Ser Gly Ser Arg Asp Ala Thr Leu 355 360 365

Arg Val Trp Asp Ile Glu Thr Gly Gln Cys Leu His Val Leu Met Gly 370 375 380

His Val Ala Ala Val Arg Cys Val Gln Tyr Asp Gly Arg Arg Val Val
385 390 395 400

Ser Gly Ala Tyr Asp Phe Met Val Lys Val Trp Asp Pro Glu Thr Glu
405 410 415

Thr Cys Leu His Thr Leu Gln Gly His Thr Asn Arg Val Tyr Ser Leu 420 425 430

Gln Phe Asp Gly Ile His Val Val Ser Gly Ser Leu Asp Thr Ser Ile
435
440
445

Arg Val Trp Asp Val Glu Thr Gly Asn Cys Ile His Thr Leu Thr Gly
450 455 460

His Gln Ser Leu Thr Ser Gly Met Glu Leu Lys Asp Asn Ile Leu Val 465 470 475 480

Ser Gly Asn Ala Asp Ser Thr Val Lys Ile Trp Asp Ile Lys Thr Gly
485 490 495

Gln Cys Leu Gln Thr Leu Gln Gly Pro Asn Lys His Gln Ser Ala Val

Thr Cys Leu Gln Phe Asn Lys Asn Phe Val Ile Thr Ser Ser Asp Asp 515 520 525

Gly Thr Val Lys Leu Trp Asp Leu Lys Thr Gly Glu Phe Ile Arg Asn 530 535 540

Leu Val Thr Leu Glu Ser Gly Gly Ser Gly Gly Val Val Trp Arg Ile 545 550 555 560

Arg Ala Ser Asn Thr Lys Leu Val Cys Ala Val Gly Ser Arg Asn Gly
565 570 575

Thr Glu Glu Thr Lys Leu Leu Val Leu Asp Phe Asp Val Asp Met Lys
580 585 590

<210> 5

<211> 553

<212> PRT

<213> Homo sapiens

<400> 5

Met Gly Phe Tyr Gly Thr Leu Lys Met Ile Phe Tyr Lys Met Lys Arg

1 5 10 15

Lys Leu Asp His Gly Ser Glu Val Arg Ser Phe Ser Leu Gly Lys Lys 20 25 30

Pro Cys Lys Val Ser Glu Tyr Thr Ser Thr Thr Gly Leu Val Pro Cys
35 40 45

Ser Ala Thr Pro Thr Thr Phe Gly Asp Leu Arg Ala Ala Asn Gly Gln
50 55 60

Gly Gln Gln Arg Arg Ile Thr Ser Val Gln Pro Pro Thr Gly Leu
65 70 75 80

Gln Glu Trp Leu Lys Met Phe Gln Ser Trp Ser Gly Pro Glu Lys Leu

85 90 95

Leu Ala Leu Asp Glu Leu Ile Asp Ser Cys Glu Pro Thr Gln Val Lys

100 105 110 110

His Met Met Gln Val Ile Glu Pro Gln Phe Gln Arg Asp Phe Ile Ser 115 120 125 Leu Leu Pro Lys Glu Leu Ala Leu Tyr Val Leu Ser Phe Leu Glu Pro 130 135 140

Lys Asp Leu Leu Gln Ala Ala Gln Thr Cys Arg Tyr Trp Arg Ile Leu 145 150 155 160

Ala Glu Asp Asn Leu Leu Trp Arg Glu Lys Cys Lys Glu Glu Gly Ile 165 170 175

Asp Glu Pro Leu His Ile Lys Arg Arg Lys Val Ile Lys Pro Gly Phe 180 185 190

Ile His Ser Pro Trp Lys Ser Ala Tyr Ile Arg Gln His Arg Ile Asp 195 200 205

Thr Asn Trp Arg Arg Gly Glu Leu Lys Ser Pro Lys Val Leu Lys Gly
210 215 220

His Asp Asp His Val Ile Thr Cys Leu Gln Phe Cys Gly Asn Arg Ile
225 230 235 240

Val Ser Gly Ser Asp Asp Asn Thr Leu Lys Val Trp Ser Ala Val Thr
245 250 255

Gly Lys Cys Leu Arg Thr Leu Val Gly His Thr Gly Gly Val Trp Ser 260 265 270

Ser Gln Met Arg Asp Asn Ile Ile Ile Ser Gly Ser Thr Asp Arg Thr
275 280 285

Leu Lys Val Trp Asn Ala Glu Thr Gly Glu Cys Ile His Thr Leu Tyr
290 295 300

Gly His Thr Ser Thr Val Arg Cys Met His Leu His Glu Lys Arg Val

305 310 315 320

Val Ser Gly Ser Arg Asp Ala Thr Leu Arg Val Trp Asp Ile Glu Thr
325 330 335

Gly Gln Cys Leu His Val Leu Met Gly His Val Ala Ala Val Arg Cys 340 345 350

Val Gln Tyr Asp Gly Arg Arg Val Val Ser Gly Ala Tyr Asp Phe Met 355 360 365

Val Lys Val Trp Asp Pro Glu Thr Glu Thr Cys Leu His Thr Leu Gln 370 375 380

Gly His Thr Asn Arg Val Tyr Ser Leu Gln Phe Asp Gly Ile His Val
385 390 395 400

Val Ser Gly Ser Leu Asp Thr Ser Ile Arg Val Trp Asp Val Glu Thr
405 410 415

Gly Asn Cys Ile His Thr Leu Thr Gly His Gln Ser Leu Thr Ser Gly
420 425 430

Met Glu Leu Lys Asp Asn Ile Leu Val Ser Gly Asn Ala Asp Ser Thr
435 440 445

Val Lys Ile Trp Asp Ile Lys Thr Gly Gln Cys Leu Gln Thr Leu Gln
450 455 460

Gly Pro Asn Lys His Gln Ser Ala Val Thr Cys Leu Gln Phe Asn Lys
465 470 475 480

Asn Phe Val Ile Thr Ser Ser Asp Asp Gly Thr Val Lys Leu Trp Asp
485 490 495

Leu Lys Thr Gly Glu Phe Ile Arg Asn Leu Val Thr Leu Glu Ser Gly 500 505 510

Gly Ser Gly Gly Val Val Trp Arg Ile Arg Ala Ser Asn Thr Lys Leu 515 520 525

Val Cys Ala Val Gly Ser Arg Asn Gly Thr Glu Glu Thr Lys Leu Leu 530 535 540

Val Leu Asp Phe Asp Val Asp Met Lys

545 550

<210> 6

<211> 545

<212> PRT

<213> Homo sapiens

<400> 6

Met Ile Phe Tyr Lys Met Lys Arg Lys Leu Asp His Gly Ser Glu Val

Arg Ser Phe Ser Leu Gly Lys Lys Pro Cys Lys Val Ser Glu Tyr Thr

Ser Thr Thr Gly Leu Val Pro Cys Ser Ala Thr Pro Thr Thr Phe Gly 35 40 45

Asp Leu Arg Ala Ala Asn Gly Gln Gly Gln Gln Arg Arg Ile Thr
50 55 60

Ser Val Gln Pro Pro Thr Gly Leu Gln Glu Trp Leu Lys Met Phe Gln 65 70 75 80

Ser Trp Ser Gly Pro Glu Lys Leu Leu Ala Leu Asp Glu Leu Ile Asp

85

90

95

Ser Cys Glu Pro Thr Gln Val Lys His Met Met Gln Val Ile Glu Pro 100 105 110

Gln Phe Gln Arg Asp Phe Ile Ser Leu Leu Pro Lys Glu Leu Ala Leu 115 120 125

Tyr Val Leu Ser Phe Leu Glu Pro Lys Asp Leu Leu Gln Ala Ala Gln 130 135 140

Thr Cys Arg Tyr Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu Trp Arg 145 150 155 160

Glu Lys Cys Lys Glu Glu Gly Ile Asp Glu Pro Leu His Ile Lys Arg 165 170 175

Arg Lys Val Ile Lys Pro Gly Phe Ile His Ser Pro Trp Lys Ser Ala 180 185 190

Tyr Ile Arg Gln His Arg Ile Asp Thr Asn Trp Arg Arg Gly Glu Leu
195 200 205

Lys Ser Pro Lys Val Leu Lys Gly His Asp Asp His Val Ile Thr Cys
210 220

Leu Gln Phe Cys Gly Asn Arg Ile Val Ser Gly Ser Asp Asn And Thr
225 230 235 240

Leu Lys Val Trp Ser Ala Val Thr Gly Lys Cys Leu Arg Thr Leu Val 245 250 255

Gly His Thr Gly Gly Val Trp Ser Ser Gln Met Arg Asp Asn Ile Ile
260 265 270

Ile Ser Gly Ser Thr Asp Arg Thr Leu Lys Val Trp Asn Ala Glu Thr
275 280 285

Gly Glu Cys Ile His Thr Leu Tyr Gly His Thr Ser Thr Val Arg Cys 290 295 300

Met His Leu His Glu Lys Arg Val Val Ser Gly Ser Arg Asp Ala Thr 305 310 315 320

Leu Arg Val Trp Asp Ile Glu Thr Gly Gln Cys Leu His Val Leu Met 325 330 335

Gly His Val Ala Ala Val Arg Cys Val Gln Tyr Asp Gly Arg Arg Val
340 345 350

Val Ser Gly Ala Tyr Asp Phe Met Val Lys Val Trp Asp Pro Glu Thr 355 360 365

Glu Thr Cys Leu His Thr Leu Gln Gly His Thr Asn Arg Val Tyr Ser 370 375 380

Leu Gln Phe Asp Gly Ile His Val Val Ser Gly Ser Leu Asp Thr Ser 385 390 395 400

Ile Arg Val Trp Asp Val Glu Thr Gly Asn Cys Ile His Thr Leu Thr 405 410 415

Gly His Gln Ser Leu Thr Ser Gly Met Glu Leu Lys Asp Asn Ile Leu
420 425 430

Val Ser Gly Asn Ala Asp Ser Thr Val Lys Ile Trp Asp Ile Lys Thr

435 440 445

Gly Gln Cys Leu Gln Thr Leu Gln Gly Pro Asn Lys His Gln Ser Ala 450 455 460

Val Thr Cys Leu Gln Phe Asn Lys Asn Phe Val Ile Thr Ser Ser Asp 465 470 475 480

Asp Gly Thr Val Lys Leu Trp Asp Leu Lys Thr Gly Glu Phe Ile Arg
485 490 495

Asn Leu Val Thr Leu Glu Ser Gly Gly Ser Gly Gly Val Val Trp Arg 500 505 510

Ile Arg Ala Ser Asn Thr Lys Leu Val Cys Ala Val Gly Ser Arg Asn 515 520 525

Gly Thr Glu Glu Thr Lys Leu Leu Val Leu Asp Phe Asp Val Asp Met
530 535 540

Lys

D2

545

<210> 7

<211> 540

<212> PRT

<213> Homo sapiens

<400> 7

Met Lys Arg Lys Leu Asp His Gly Ser Glu Val Arg Ser Phe Ser Leu

1 5 10 15

Gly Lys Lys Pro Cys Lys Val Ser Glu Tyr Thr Ser Thr Thr Gly Leu

20 25 30

Val Pro Cys Ser Ala Thr Pro Thr Thr Phe Gly Asp Leu Arg Ala Ala 35 40 45

Asn Gly Gln Gly Gln Gln Arg Arg Ile Thr Ser Val Gln Pro Pro 50 55 60

Thr Gly Leu Gln Glu Trp Leu Lys Met Phe Gln Ser Trp Ser Gly Pro
65 70 75 80

Glu Lys Leu Leu Ala Leu Asp Glu Leu Ile Asp Ser Cys Glu Pro Thr

85 90 95

Gln Val Lys His Met Met Gln Val Ile Glu Pro Gln Phe Gln Arg Asp 100 105 110

Phe Ile Ser Leu Leu Pro Lys Glu Leu Ala Leu Tyr Val Leu Ser Phe 115 120 125

Leu Glu Pro Lys Asp Leu Leu Gln Ala Ala Gln Thr Cys Arg Tyr Trp

130 135 140

Arg Ile Leu Ala Glu Asp Asn Leu Leu Trp Arg Glu Lys Cys Lys Glu
145 150 155 160

Glu Gly Ile Asp Glu Pro Leu His Ile Lys Arg Arg Lys Val Ile Lys

165 170 175

Pro Gly Phe Ile His Ser Pro Trp Lys Ser Ala Tyr Ile Arg Gln His 180 185 190

Arg Ile Asp Thr Asn Trp Arg Gly Glu Leu Lys Ser Pro Lys Val 195 200 205 Leu Lys Gly His Asp Asp His Val Ile Thr Cys Leu Gln Phe Cys Gly
210 215 220

Asn Arg Ile Val Ser Gly Ser Asp Asp Asn Thr Leu Lys Val Trp Ser 225 230 235 240

Ala Val Thr Gly Lys Cys Leu Arg Thr Leu Val Gly His Thr Gly Gly
245 250 255

Val Trp Ser Ser Gln Met Arg Asp Asn Ile Ile Ile Ser Gly Ser Thr
260 265 270

Asp Arg Thr Leu Lys Val Trp Asn Ala Glu Thr Gly Glu Cys Ile His
275 280 285

Thr Leu Tyr Gly His Thr Ser Thr Val Arg Cys Met His Leu His Glu 290 295 300

Lys Arg Val Val Ser Gly Ser Arg Asp Ala Thr Leu Arg Val Trp Asp 305 310 315 320

Ile Glu Thr Gly Gln Cys Leu His Val Leu Met Gly His Val Ala Ala
325 330 335

Val Arg Cys Val Gln Tyr Asp Gly Arg Arg Val Val Ser Gly Ala Tyr 340 345 350

Asp Phe Met Val Lys Val Trp Asp Pro Glu Thr Glu Thr Cys Leu His
355 360 365

Thr Leu Gln Gly His Thr Asn Arg Val Tyr Ser Leu Gln Phe Asp Gly 370 375 380

Ile His Val Val Ser Gly Ser Leu Asp Thr Ser Ile Arg Val Trp Asp
385 390 395 400

Val Glu Thr Gly Asn Cys Ile His Thr Leu Thr Gly His Gln Ser Leu
405 410 415

Thr Ser Ġly Met Glu Leu Lys Asp Asn Ile Leu Val Ser Gly Asn Ala 420 425 430

Asp Ser Thr Val Lys Ile Trp Asp Ile Lys Thr Gly Gln Cys Leu Gln
435
440
445

Thr Leu Gln Gly Pro Asn Lys His Gln Ser Ala Val Thr Cys Leu Gln 450 455 460

Phe Asn Lys Asn Phe Val Ile Thr Ser Ser Asp Asp Gly Thr Val Lys
465 470 475 480

Leu Trp Asp Leu Lys Thr Gly Glu Phe Ile Arg Asn Leu Val Thr Leu
485 490 495

Glu Ser Gly Gly Ser Gly Gly Val Val Trp Arg Ile Arg Ala Ser Asn
500 505 510

Thr Lys Leu Val Cys Ala Val Gly Ser Arg Asn Gly Thr Glu Glu Thr
515 520 525

Lys Leu Leu Val Leu Asp Phe Asp Val Asp Met Lys 530 540

<210> 8

<211> 589

<212> PRT

<213> Homo sapiens

<400> 8

Met Ser Lys Pro Gly Lys Pro Thr Leu Asn His Gly Leu Val Pro Val

1 5 10 15

Asp Leu Lys Ser Ala Lys Glu Pro Leu Pro His Gln Thr Val Met Lys
20 25 30

Ile Phe Ser Ile Ser Ile Ile Ala Gln Gly Leu Pro Phe Cys Arg Arg
35 40 45

Arg Met Lys Arg Lys Leu Asp His Gly Ser Glu Val Arg Ser Phe Ser 50 55 60

Leu Gly Lys Lys Pro Cys Lys Val Ser Glu Tyr Thr Ser Thr Thr Gly
65 70 75 80

Leu Val Pro Cys Ser Ala Thr Pro Thr Thr Phe Gly Asp Leu Arg Ala 85 90 95

Ala Asn Gly Gln Gln Gln Arg Arg Ile Thr Ser Val Gln Pro 100 105 110

Pro Thr Gly Leu Gln Glu Trp Leu Lys Met Phe Gln Ser Trp Ser Gly
115 120 125

Pro Glu Lys Leu Leu Ala Leu Asp Glu Leu Ile Asp Ser Cys Glu Pro 130 135 140

Thr Gln Val Lys His Met Met Gln Val Ile Glu Pro Gln Phe Gln Arg
145 150 150 155 160

Asp Phe Ile Ser Leu Leu Pro Lys Glu Leu Ala Leu Tyr Val Leu Ser

165 170 175

Phe Leu Glu Pro Lys Asp Leu Leu Gln Ala Ala Gln Thr Cys Arg Tyr
180 185 190

Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu Trp Arg Glu Lys Cys Lys
195 200 205

Glu Glu Gly Ile Asp Glu Pro Leu His Ile Lys Arg Arg Lys Val Ile 210 215 220

Lys Pro Gly Phe Ile His Ser Pro Trp Lys Ser Ala Tyr Ile Arg Gln 225 230 235 240

His Arg Ile Asp Thr Asn Trp Arg Arg Gly Glu Leu Lys Ser Pro Lys
245 250 255

Val Leu Lys Gly His Asp Asp His Val Ile Thr Cys Leu Gln Phe Cys
260 265 270

Gly Asn Arg Ile Val Ser Gly Ser Asp Asn Thr Leu Lys Val Trp
275 280 285

Ser Ala Val Thr Gly Lys Cys Leu Arg Thr Leu Val Gly His Thr Gly 290 295 300

Gly Val Trp Ser Ser Gln Met Arg Asp Asn Ile Ile Ile Ser Gly Ser 305 310 315 320

Thr Asp Arg Thr Leu Lys Val Trp Asn Ala Glu Thr Gly Glu Cys Ile 325 330 335

His Thr Leu Tyr Gly His Thr Ser Thr Val Arg Cys Met His Leu His 340 345 350

Glu Lys Arg Val Val Ser Gly Ser Arg Asp Ala Thr Leu Arg Val Trp

355 360 365

Asp Ile Glu Thr Gly Gln Cys Leu His Val Leu Met Gly His Val Ala 370 375 380

Ala Val Arg Cys Val Gln Tyr Asp Gly Arg Arg Val Val Ser Gly Ala
385 390 395 400

Tyr Asp Phe Met Val Lys Val Trp Asp Pro Glu Thr Glu Thr Cys Leu
405 410 415

His Thr Leu Gln Gly His Thr Asn Arg Val Tyr Ser Leu Gln Phe Asp
420 425 430

Gly Ile His Val Val Ser Gly Ser Leu Asp Thr Ser Ile Arg Val Trp
435 440 445

Asp Val Glu Thr Gly Asn Cys Ile His Thr Leu Thr Gly His Gln Ser
450 455 460

Leu Thr Ser Gly Met Glu Leu Lys Asp Asn Ile Leu Val Ser Gly Asn 465 470 475 480

Ala Asp Ser Thr Val Lys Ile Trp Asp Ile Lys Thr Gly Gln Cys Leu
485 490 495

Gln Thr Leu Gln Gly Pro Asn Lys His Gln Ser Ala Val Thr Cys Leu 500 505 510

Gln Phe Asn Lys Asn Phe Val Ile Thr Ser Ser Asp Asp Gly Thr Val
515 520 525

Lys Leu Trp Asp Leu Lys Thr Gly Glu Phe Ile Arg Asn Leu Val Thr 530 535 540

Leu Glu Ser Gly Gly Ser Gly Gly Val Val Trp Arg Ile Arg Ala Ser 545 550 555 560

Asn Thr Lys Leu Val Cys Ala Val Gly Ser Arg Asn Gly Thr Glu Glu 565 570 575

Thr Lys Leu Leu Val Leu Asp Phe Asp Val Asp Met Lys 580 585

<210> 9

<211> 559

<212> PRT

<213> Homo sapiens

<400> 9

Met Lys Ile Phe Ser Ile Ser Ile Ile Ala Gln Gly Leu Pro Phe Cys

1 5 10 15

Arg Arg Met Lys Arg Lys Leu Asp His Gly Ser Glu Val Arg Ser
20 25 30

Phe Ser Leu Gly Lys Lys Pro Cys Lys Val Ser Glu Tyr Thr Ser Thr

35 40 45

Thr Gly Leu Val Pro Cys Ser Ala Thr Pro Thr Thr Phe Gly Asp Leu 50 55 60

Arg Ala Ala Asn Gly Gln Gly Gln Arg Arg Ile Thr Ser Val
65 70 75 80

Gln Pro Pro Thr Gly Leu Gln Glu Trp Leu Lys Met Phe Gln Ser Trp

85 90 95

Ser Gly Pro Glu Lys Leu Leu Ala Leu Asp Glu Leu Ile Asp Ser Cys
100 105 110

Glu Pro Thr Gln Val Lys His Met Met Gln Val Ile Glu Pro Gln Phe 115 120 125

Gln Arg Asp Phe Ile Ser Leu Leu Pro Lys Glu Leu Ala Leu Tyr Val 130 135 140

Leu Ser Phe Leu Glu Pro Lys Asp Leu Leu Gln Ala Ala Gln Thr Cys
145 150 155 160

Arg Tyr Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu Trp Arg Glu Lys

165 170 175

Cys Lys Glu Glu Gly Ile Asp Glu Pro Leu His Ile Lys Arg Arg Lys 180 185 190

Val Ile Lys Pro Gly Phe Ile His Ser Pro Trp Lys Ser Ala Tyr Ile.

195 200 205

Arg Gln His Arg Ile Asp Thr Asn Trp Arg Arg Gly Glu Leu Lys Ser 210 215 220

Pro Lys Val Leu Lys Gly His Asp Asp His Val Ile Thr Cys Leu Gln 225 230 235 240

Phe Cys Gly Asn Arg Ile Val Ser Gly Ser Asp Asp Asn Thr Leu Lys
245 250 255

Val Trp Ser Ala Val Thr Gly Lys Cys Leu Arg Thr Leu Val Gly His

260 265 270

Thr Gly Gly Val Trp Ser Ser Gln Met Arg Asp Asn Ile Ile Ile Ser 275 280 285

Gly Ser Thr Asp Arg Thr Leu Lys Val Trp Asn Ala Glu Thr Gly Glu 290 295 300

Cys Ile His Thr Leu Tyr Gly His Thr Ser Thr Val Arg Cys Met His 305 310 315 320

Leu His Glu Lys Arg Val Val Ser Gly Ser Arg Asp Ala Thr Leu Arg 325 330 335

Val Trp Asp Ile Glu Thr Gly Gln Cys Leu His Val Leu Met Gly His
340 345 350

N

Val Ala Ala Val Arg Cys Val Gln Tyr Asp Gly Arg Arg Val Val Ser 355 360 365

Gly Ala Tyr Asp Phe Met Val Lys Val Trp Asp Pro Glu Thr Glu Thr 370 375 380

Cys Leu His Thr Leu Gln Gly His Thr Asn Arg Val Tyr Ser Leu Gln 385

Phe Asp Gly Ile His Val Val Ser Gly Ser Leu Asp Thr Ser Ile Arg 405 410 415

Val Trp Asp Val Glu Thr Gly Asn Cys Ile His Thr Leu Thr Gly His
420 425 430

Gln Ser Leu Thr Ser Gly Met Glu Leu Lys Asp Asn Ile Leu Val Ser
435 440 445

Gly Asn Ala Asp Ser Thr Val Lys Ile Trp Asp Ile Lys Thr Gly Gln
450 455 460

Cys Leu Gln Thr Leu Gln Gly Pro Asn Lys His Gln Ser Ala Val Thr
465 470 475 480

Cys Leu Gln Phe Asn Lys Asn Phe Val Ile Thr Ser Ser Asp Asp Gly
485 490 495

Thr Val Lys Leu Trp Asp Leu Lys Thr Gly Glu Phe Ile Arg Asn Leu 500 505 510

Val Thr Leu Glu Ser Gly Gly Ser Gly Gly Val Val Trp Arg Ile Arg
515 520 525

Ala Ser Asn Thr Lys Leu Val Cys Ala Val Gly Ser Arg Asn Gly Thr
530 535 540

Glu Glu Thr Lys Leu Leu Val Leu Asp Phe Asp Val Asp Met Lys
545 550 555

<210> 10

<211> 540

<212> PRT

<213> Homo sapiens

<400> 10

Met Lys Arg Lys Leu Asp His Gly Ser Glu Val Arg Ser Phe Ser Leu

1 5 10 15

Gly Lys Lys Pro Cys Lys Val Ser Glu Tyr Thr Ser Thr Thr Gly Leu 20 25 30

Val Pro Cys Ser Ala Thr Pro Thr Thr Phe Gly Asp Leu Arg Ala Ala
35 40 45

Asn Gly Gln Gly Gln Gln Arg Arg Ile Thr Ser Val Gln Pro Pro
50 55 60

Thr Gly Leu Gln Glu Trp Leu Lys Met Phe Gln Ser Trp Ser Gly Pro
65 70 75 80

Glu Lys Leu Leu Ala Leu Asp Glu Leu Ile Asp Ser Cys Glu Pro Thr

85 90 95

Gln Val Lys His Met Met Gln Val Ile Glu Pro Gln Phe Gln Arg Asp 100 105 110

Phe Ile Ser Leu Leu Pro Lys Glu Leu Ala Leu Tyr Val Leu Ser Phe 115 120 125

Leu Glu Pro Lys Asp Leu Leu Gln Ala Ala Gln Thr Cys Arg Tyr Trp

130 135 140

Glu Gly Ile Asp Glu Pro Leu His Ile Lys Arg Arg Lys Val Ile Lys

165 170 175

Pro Gly Phe Ile His Ser Pro Trp Lys Ser Ala Tyr Ile Arg Gln His
180 185 190

Arg Ile Asp Thr Asn Trp Arg Gly Glu Leu Lys Ser Pro Lys Val
195 200 205

Leu Lys Gly His Asp Asp His Val Ile Thr Cys Leu Gln Phe Cys Gly
210 215 220

Asn Arg Ile Val Ser Gly Ser Asp Asn Thr Leu Lys Val Trp Ser 225 230 235 240

Ala Val Thr Gly Lys Cys Leu Arg Thr Leu Val Gly His Thr Gly Gly
245 250 255

Val Trp Ser Ser Gln Met Arg Asp Asn Ile Ile Ile Ser Gly Ser Thr
260 265 270

Asp Arg Thr Leu Lys Val Trp Asn Ala Glu Thr Gly Glu Cys Ile His
275 280 285

Thr Leu Tyr Gly His Thr Ser Thr Val Arg Cys Met His Leu His Glu 290 295 300

Lys Arg Val Val Ser Gly Ser Arg Asp Ala Thr Leu Arg Val Trp Asp 305 310 315 320

Ile Glu Thr Gly Gln Cys Leu His Val Leu Met Gly His Val Ala Ala
325 330 335

Val Arg Cys Val Gln Tyr Asp Gly Arg Arg Val Val Ser Gly Ala Tyr 340 345 350

Asp Phe Met Val Lys Val Trp Asp Pro Glu Thr Glu Thr Cys Leu His
355 360 365

Thr Leu Gln Gly His Thr Asn Arg Val Tyr Ser Leu Gln Phe Asp Gly
370 375 380

Ile His Val Val Ser Gly Ser Leu Asp Thr Ser Ile Arg Val Trp Asp

385 390 395 400

Val Glu Thr Gly Asn Cys Ile His Thr Leu Thr Gly His Gln Ser Leu 405 410 415

Thr Ser Gly Met Glu Leu Lys Asp Asn Ile Leu Val Ser Gly Asn Ala
420 425 430

Asp Ser Thr Val Lys Ile Trp Asp Ile Lys Thr Gly Gln Cys Leu Gln 435 440 445

Thr Leu Gln Gly Pro Asn Lys His Gln Ser Ala Val Thr Cys Leu Gln 450 455 460

Phe Asn Lys Asn Phe Val Ile Thr Ser Ser Asp Asp Gly Thr Val Lys
465 470 475 480

Leu Trp Asp Leu Lys Thr Gly Glu Phe Ile Arg Asn Leu Val Thr Leu
485 490 495

Glu Ser Gly Gly Ser Gly Gly Val Val Trp Arg Ile Arg Ala Ser Asn
500 505 510

Thr Lys Leu Val Cys Ala Val Gly Ser Arg Asn Gly Thr Glu Glu Thr
515 520 525

Lys Leu Leu Val Leu Asp Phe Asp Val Asp Met Lys 530 535

<210> 11

<211> 34

<212> DNA

<213> Artificial Sequence

	<220>		
	<223>	Description of Artificial Sequence:	
		Oligonucleotide primer	
	<400>	11	
	cgggat	ccac catggatgat ggatcgatga cacc	34
	<210>	12	
	<211>	33	
	<212>	DNA	
	<213>	Artificial Sequence	
	<220>		
	<223>	Description of Artificial Sequence:	
		Oligonucleotide primer	
2			
	<400>		2.2
	ggaatt	cctt aagggtatac agcatcaaag tcg	33
	<210>		
	<211>		
	<212>		
	<213>	Artificial Sequence	
	<220>		
		Description of Artificial Sequence:	
	<223>	Oligonucleotide primer	
		Oligonacieotiae primer	
	<400>	13	
		tcatg tccacatcaa agtcc	25
	<210>	14	
	∠211 >		

<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Description of Artificial Sequence:	
	Oligonucleotide primer	
<400>	14	
ggtaa	ttaca agttcttgtt gaactg	26
<210>	15	
<211>	22	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Description of Artificial Sequence:	
	Oligonucleotide primer	
<400>	15	
ccctg	caacg tgtgtagaca gg	22
<210>		
<211>		
<212>		
<213>	Artificial Sequence	
.000		
<220>	Description of Authoritation Company	
<223>	Description of Artificial Sequence:	
	Oligonucleotide primer	
-400:	16	
<400>		24
ccagt	ctctg cattccacac tttg	4

<210>	17	
<211>	23	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Description of Artificial Sequence:	
	Oligonucleotide primer	
<400>		
ctcaga	acagg tcaggacatt tgg	23
<210>	10	
<211>		
<212>		
	Artificial Sequence	
<220>		
<223>	Description of Artificial Sequence:	
	Oligonucleotide primer	
<400>	18 .	
ggaat	tccat gaaaagattg gaccatggtt ctg	33
<210>		
<211>		
<212>		
<213>	Artificial Sequence	
<220>	•	
	Description of Artificial Sequence:	
	Oligonucleotide primer	
	-	
<400>	19	

<210> 20

<211> 1881

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: 6 myc tagged homo sapiens

<400> 20

atggagcaaa agctcatttc tgaagaggac ttgaatgaaa tggagcaaaa gctcatttct 60 gaagaggact tgaatgaaat ggagcaaaag ctcatttctg aagaggactt gaatgaaatg 120 gagcaaaagc tcatttctga agaggacttg aatgaaatgg agcaaaagct catttctgaa 180 gaggacttga atgaaatgga gagcttgggc gacctcacca tggagcaaaa gctcatttct 240 gaagaggact tgaattccat gaaaagaaag ttggaccatg gttctgaggt ccgctctttt 300 tctttgggaa agaaaccatg caaagtctca gaatatacaa gtaccactgg gcttgtacca 360 tgttcagcaa caccaacaac ttttggggac ctcagagcag ccaatggcca agggcaacaa 420 cgacgccgaa ttacatctgt ccagccacct acaggcctcc aggaatggct aaaaatgttt 480 cagagctgga gtggaccaga gaaattgctt gctttagatg aactcattga tagttgtgaa 540 ccaacacaag taaaacatat gatgcaagtg atagaacccc agtttcaacg agacttcatt 600 tcattgctcc ctaaagagtt ggcactctat gtgctttcat tcctggaacc caaagacctg 660 ctacaagcag ctcagacatg tcgctactgg agaattttgg ctgaagacaa ccttctctgg 720 agagagaaat gcaaagaaga ggggattgat gaaccattgc acatcaagag aagaaaagta 780 ataaaaccag gtttcataca cagtccatgg aaaagtgcat acatcagaca gcacagaatt 840 gatactaact ggaggcgagg agaactcaaa tctcctaagg tgctgaaagg acatgatgat 900 catgtgatca catgcttaca gttttgtggt aaccgaatag ttagtggttc tgatgacaac 960 actttaaaag tttggtcagc agtcacaggc aaatgtctga gaacattagt gggacataca 1020 ggtggagtat ggtcatcaca aatgagggac aacatcatca ttagtggatc tacagatcgg 1080 acactcaaag tgtggaatgc agagactgga gaatgtatac acaccttata tgggcatact 1140 tccactgtgc gttgtatgca tcttcatgaa aaaagagttg ttagcggttc tcgagatgcc 1200 actcttaggg tttgggatat tgagacaggc cagtgtttac atgttttgat gggtcatgtt 1260 gcagcagtcc gctgtgttca atatgatggc aggagggttg ttagtggagc atatgatttt 1320





atggtaaagg tgtgggatcc agagactgaa acctgtctac acacgttgca ggggcatact 1380 aatagagtct attcattaca gtttgatggt atccatgtgg tgagtggatc tcttgataca 1440 tccatccgtg tttgggatgt ggagacaggg aattgcattc acacgttaac agggcaccag 1500 tcgttaacaa gtggaatgga actcaaagac aatattcttg tctctgggaa tgcagattct 1560 acagttaaaa tctgggatat caaaacagga cagtgtttac aaacattgca aggtcccaac 1620 aagcatcaga gtgctgtgac ctgtttacag ttcaacaaga actttgtaat taccagctca 1680 gatgatggaa ctgtaaaact atgggacttg aaaacgggtg aatttattcg aaacctagtc 1740 acattggaga gtgggggag tgggggagtt gtgtggcgga tcagagcctc aaaacaaag 1800 ctggtgtgt cagttgggag tcggaatggg actgaagaaa ccaagctgct ggtgctggac 1860 tttgatgtgg acatgaagtg a

<210> 21

<211> 626

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: 6 myc tagged homo sapien

<400> 21

Met Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Glu Met Glu Gln

1 5 10 15

Lys Leu Ile Ser Glu Glu Asp Leu Asn Glu Met Glu Gln Lys Leu Ile
20 25 30

Ser Glu Glu Asp Leu Asn Glu Met Glu Gln Lys Leu Ile Ser Glu Glu
35 40 45

Asp Leu Asn Glu Met Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn 50 55 60

Glu Met Glu Ser Leu Gly Asp Leu Thr Met Glu Gln Lys Leu Ile Ser

65 70 75 80

Glu Glu Asp Leu Asn Ser Met Lys Arg Lys Leu Asp His Gly Ser Glu 85 90 95

Val Arg Ser Phe Ser Leu Gly Lys Lys Pro Cys Lys Val Ser Glu Tyr

100 105 110

Thr Ser Thr Thr Gly Leu Val Pro Cys Ser Ala Thr Pro Thr Thr Phe
115 120 125

Gly Asp Leu Arg Ala Ala Asn Gly Gln Gly Gln Gln Arg Arg Ile
130 135 140

Thr Ser Val Gln Pro Pro Thr Gly Leu Gln Glu Trp Leu Lys Met Phe
145 150 155 160

Gln Ser Trp Ser Gly Pro Glu Lys Leu Leu Ala Leu Asp Glu Leu Ile 165 170 175

Asp Ser Cys Glu Pro Thr Gln Val Lys His Met Met Gln Val Ile Glu 180 185 190

Pro Gln Phe Gln Arg Asp Phe Ile Ser Leu Leu Pro Lys Glu Leu Ala 195 200 205

Leu Tyr Val Leu Ser Phe Leu Glu Pro Lys Asp Leu Leu Gln Ala Ala 210 215 220

Gln Thr Cys Arg Tyr Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu Trp
225 230 235 240

Arg Glu Lys Cys Lys Glu Glu Gly Ile Asp Glu Pro Leu His Ile Lys
245 250 255

Arg Arg Lys Val Ile Lys Pro Gly Phe Ile His Ser Pro Trp Lys Ser 260 265 270

Ala Tyr Ile Arg Gln His Arg Ile Asp Thr Asn Trp Arg Arg Gly Glu 275 280 285

Leu Lys Ser Pro Lys Val Leu Lys Gly His Asp Asp His Val Ile Thr
290 295 300

Cys Leu Gln Phe Cys Gly Asn Arg Ile Val Ser Gly Ser Asp Asn Asn 305 310 315 320

Thr Leu Lys Val Trp Ser Ala Val Thr Gly Lys Cys Leu Arg Thr Leu 325 330 335

Val Gly His Thr Gly Gly Val Trp Ser Ser Gln Met Arg Asp Asn Ile 340 345 350

Ile Ile Ser Gly Ser Thr Asp Arg Thr Leu Lys Val Trp Asn Ala Glu 355 360 365

Thr Gly Glu Cys Ile His Thr Leu Tyr Gly His Thr Ser Thr Val Arg 370 375 380

Cys Met His Leu His Glu Lys Arg Val Val Ser Gly Ser Arg Asp Ala 385 390 395 400

Thr Leu Arg Val Trp Asp Ile Glu Thr Gly Gln Cys Leu His Val Leu
405 410 415

Met Gly His Val Ala Ala Val Arg Cys Val Gln Tyr Asp Gly Arg Arg
420 425 430

Val Val Ser Gly Ala Tyr Asp Phe Met Val Lys Val Trp Asp Pro Glu
435 440 445

Thr Glu Thr Cys Leu His Thr Leu Gln Gly His Thr Asn Arg Val Tyr 450 455 460

Ser Leu Gln Phe Asp Gly Ile His Val Val Ser Gly Ser Leu Asp Thr 465 470 475 480

Ser Ile Arg Val Trp Asp Val Glu Thr Gly Asn Cys Ile His Thr Leu
485 490 495

Thr Gly His Gln Ser Leu Thr Ser Gly Met Glu Leu Lys Asp Asn Ile
500 505 510

Leu Val Ser Gly Asn Ala Asp Ser Thr Val Lys Ile Trp Asp Ile Lys
515 520 525

Thr Gly Gln Cys Leu Gln Thr Leu Gln Gly Pro Asn Lys His Gln Ser 530 535 540

Ala Val Thr Cys Leu Gln Phe Asn Lys Asn Phe Val Ile Thr Ser Ser 545 550 550 560

Asp Asp Gly Thr Val Lys Leu Trp Asp Leu Lys Thr Gly Glu Phe Ile 565 570 575

Arg Asn Leu Val Thr Leu Glu Ser Gly Gly Ser Gly Gly Val Val Trp
580 585 590

Arg Ile Arg Ala Ser Asn Thr Lys Leu Val Cys Ala Val Gly Ser Arg
595 600 605

Asn Gly Thr Glu Glu Thr Lys Leu Leu Val Leu Asp Phe Asp Val Asp

610 615 620

Met Lys

625

<210> 22

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide primer

<400> 22

gggtacccct cattattccc tcgagttctt c

general contraction of the contr

31

29

<210> 23

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide primer

<400> 23

ggaattcctt catgtccaca tcaaagtcc

<210> 24

<211> 2010

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: V5HIS tagged
homo sapien

<400> 24

atgtgtgtcc cgagaagcgg tttgatactg agctgcattt gcctttactg tggagttttg 60 ttgccggttc tgctccctaa tcttcctttt ctgacgtgcc tgagcatgtc cacattagaa 120 tctgtgacat acctacctga aaaaggttta tattgtcaga gactgccaag cagccggaca 180 cacgggggca cagaatcact gaaggggaaa aatacagaaa atatgggttt ctacggcaca 240 ttaaaaatga ttttttacaa aatgaaaaga aagttggacc atggttctga ggtccgctct 300 ttttctttgg gaaagaaacc atgcaaagtc tcagaatata caagtaccac tgggcttgta 360 ccatgttcag caacaccaac aacttttggg gacctcagag cagccaatgg ccaagggcaa 420 caacgacgcc gaattacatc tgtccagcca cctacaggcc tccaggaatg gctaaaaatg 480 tttcagagct ggagtggacc agagaaattg cttgctttag atgaactcat tgatagttgt 540 gaaccaacac aagtaaaaca tatgatgcaa gtgatagaac cccagtttca acgagacttc 600 atttcattgc tccctaaaga gttggcactc tatgtgcttt cattcctgga acccaaagac 660 ctgctacaag cagctcagac atgtcgctac tggagaattt tggctgaaga caaccttctc 720 tggagagaga aatgcaaaga agaggggatt gatgaaccat tgcacatcaa gagaagaaaa 780 gtaataaaac caggtttcat acacagtcca tggaaaagtg catacatcag acagcacaga 840 attgatacta actggaggcg aggagaactc aaatctccta aggtgctgaa aggacatgat 900 gatcatgtga tcacatgctt acagttttgt ggtaaccgaa tagttagtgg ttctgatgac 960 aacactttaa aagtttggtc agcagtcaca ggcaaatgtc tgagaacatt agtgggacat 1020 acaggtggag tatggtcatc acaaatgaga gacaacatca tcattagtgg atctacagat 1080 cggacactca aagtgtggaa tgcagagact ggagaatgta tacacacctt atatgggcat 1140 acttccactg tgcgttgtat gcatcttcat gaaaaaagag ttgttagcgg ttctcgagat 1200 gccactctta gggtttggga tattgagaca ggccagtgtt tacatgtttt gatgggtcat 1260 gttgcagcag tccgctgtgt tcaatatgat ggcaggaggg ttgttagtgg agcatatgat 1320 tttatggtaa aggtgtggga tccagagact gaaacctgtc tacacacgtt gcaggggcat 1380 actaatagag totattoatt acagtttgat ggtatocatg tggtgagtgg atotottgat 1440 acatcaatcc gtgtttggga tgtggagaca gggaattgca ttcacacgtt aacagggcac 1500 cagtcgttaa caagtggaat ggaactcaaa gacaatattc ttgtctctgg gaatgcagat 1560 tctacagtta aaatctggga tatcaaaaca ggacagtgtt tacaaacatt gcaaggtccc 1620 aacaagcatc agagtgctgt gacctgttta cagttcaaca agaactttgt aattaccagc 1680





tcagatgatg gaactgtaaa actatgggac ttgaaaacgg gtgaatttat tcgaaaccta 1740 gtcacattgg agagtggggg gagtggggga gttgtgtggc ggatcagagc ctcaaacaca 1800 aagctggtgt gtgcagttgg gagtcggaat gggactgaag aaaccaagct gctggtgctg 1860 gactttgatg tggacatgaa ggaattctgc agatatccag cacagtggcg gccgctcgag 1920 tctagagggc ccttcgaagg taagcctatc cctaaccctc tcctcggtct cgattctacg 1980 cgtaccggtc atcatcacca tcaccattga 2010

<210> 25

<211> 669

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: V5HIS tagged homo sapien

<400> 25

Met Cys Val Pro Arg Ser Gly Leu Ile Leu Ser Cys Ile Cys Leu Tyr

1 5 10 15

Cys Gly Val Leu Leu Pro Val Leu Leu Pro Asn Leu Pro Phe Leu Thr

Cys Leu Ser Met Ser Thr Leu Glu Ser Val Thr Tyr Leu Pro Glu Lys

35 40 45

Gly Leu Tyr Cys Gln Arg Leu Pro Ser Ser Arg Thr His Gly Gly Thr
50 55 60

Glu Ser Leu Lys Gly Lys Asn Thr Glu Asn Met Gly Phe Tyr Gly Thr
65 70 75 80

Leu Lys Met Ile Phe Tyr Lys Met Lys Arg Lys Leu Asp His Gly Ser

85 90 95

Glu Val Arg Ser Phe Ser Leu Gly Lys Lys Pro Cys Lys Val Ser Glu 100 105 110

Tyr Thr Ser Thr Thr Gly Leu Val Pro Cys Ser Ala Thr Pro Thr Thr

115 120 125

Phe Gly Asp Leu Arg Ala Ala Asn Gly Gln Gly Gln Gln Arg Arg
130 135 140

Ile Thr Ser Val Gln Pro Pro Thr Gly Leu Gln Glu Trp Leu Lys Met
145 150 155 160

Phe Gln Ser Trp Ser Gly Pro Glu Lys Leu Leu Ala Leu Asp Glu Leu
165 170 175

Ile Asp Ser Cys Glu Pro Thr Gln Val Lys His Met Met Gln Val Ile 180 185 190

Glu Pro Gln Phe Gln Arg Asp Phe Ile Ser Leu Leu Pro Lys Glu Leu
195 200 205

Ala Leu Tyr Val Leu Ser Phe Leu Glu Pro Lys Asp Leu Leu Gln Ala 210 215 220

Ala Gln Thr Cys Arg Tyr Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu 225 230 235 240

Trp Arg Glu Lys Cys Lys Glu Glu Gly Ile Asp Glu Pro Leu His Ile
245 250 255

Lys Arg Arg Lys Val Ile Lys Pro Gly Phe Ile His Ser Pro Trp Lys
260 265 270

Ser Ala Tyr Ile Arg Gln His Arg Ile Asp Thr Asn Trp Arg Gly
275 280 285

Glu Leu Lys Ser Pro Lys Val Leu Lys Gly His Asp Asp His Val Ile 290 295 300

Thr Cys Leu Gln Phe Cys Gly Asn Arg Ile Val Ser Gly Ser Asp Asp 305 310 315 320

Asn Thr Leu Lys Val Trp Ser Ala Val Thr Gly Lys Cys Leu Arg Thr
325 330 335

Leu Val Gly His Thr Gly Gly Val Trp Ser Ser Gln Met Arg Asp Asn 340 345 350

Ile Ile Ile Ser Gly Ser Thr Asp Arg Thr Leu Lys Val Trp Asn Ala
355 360 365

Glu Thr Gly Glu Cys Ile His Thr Leu Tyr Gly His Thr Ser Thr Val $370 \hspace{1.5cm} 375 \hspace{1.5cm} 380$

Arg Cys Met His Leu His Glu Lys Arg Val Val Ser Gly Ser Arg Asp 385 390 395 400

Ala Thr Leu Arg Val Trp Asp Ile Glu Thr Gly Gln Cys Leu His Val $405 \hspace{1.5cm} 410 \hspace{1.5cm} 415$

Leu Met Gly His Val Ala Ala Val Arg Cys Val Gln Tyr Asp Gly Arg 420 425 430

Arg Val Val Ser Gly Ala Tyr Asp Phe Met Val Lys Val Trp Asp Pro 435 440 445

Glu Thr Glu Thr Cys Leu His Thr Leu Gln Gly His Thr Asn Arg Val

450 455 460

Tyr Ser Leu Gln Phe Asp Gly Ile His Val Val Ser Gly Ser Leu Asp 465 470 475 480

Thr Ser Ile Arg Val Trp Asp Val Glu Thr Gly Asn Cys Ile His Thr 485 490 495

Leu Thr Gly His Gln Ser Leu Thr Ser Gly Met Glu Leu Lys Asp Asn 500 505 510

Ile Leu Val Ser Gly Asn Ala Asp Ser Thr Val Lys Ile Trp Asp Ile
515 520 525

Lys Thr Gly Gln Cys Leu Gln Thr Leu Gln Gly Pro Asn Lys His Gln 530 535 540

Ser Ala Val Thr Cys Leu Gln Phe Asn Lys Asn Phe Val Ile Thr Ser 545 550 555 560

Ser Asp Asp Gly Thr Val Lys Leu Trp Asp Leu Lys Thr Gly Glu Phe
565 570 575

Ile Arg Asn Leu Val Thr Leu Glu Ser Gly Gly Ser Gly Gly Val Val
580 585 590

Trp Arg Ile Arg Ala Ser Asn Thr Lys Leu Val Cys Ala Val Gly Ser 595 600 605

Arg Asn Gly Thr Glu Glu Thr Lys Leu Leu Val Leu Asp Phe Asp Val 610 615 620

Asp Met Lys Glu Phe Cys Arg Tyr Pro Ala Gln Trp Arg Pro Leu Glu 625 630 635 640 Ser Arg Gly Pro Phe Glu Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly
645 650 655

Leu Asp Ser Thr Arg Thr Gly His His His His His His 660 665

<210> 26

<211> 2001

<212> DNA

<213> Artificial Sequence

DV

<220>

<223> Description of Artificial Sequence: MYCHIS tagged homo sapiens

<400> 26

atgtgtgtcc cgagaagcgg tttgatactg agctgcattt gcctttactg tggagttttg 60 ttgccggttc tgctccctaa tcttcctttt ctgacgtgcc tgagcatgtc cacattagaa 120 tctqtqacat acctacctga aaaaggttta tattgtcaga gactgccaag cagccggaca 180 cacgggggca cagaatcact gaaggggaaa aatacagaaa atatgggttt ctacggcaca 240 ttaaaaatga ttttttacaa aatgaaaaga aagttggacc atggttctga ggtccgctct 300 ttttctttgg gaaagaaacc atgcaaagtc tcagaatata caagtaccac tgggcttgta 360 ccatgttcag caacaccaac aacttttggg gacctcagag cagccaatgg ccaagggcaa 420 caacgacgcc gaattacatc tgtccagcca cctacaggcc tccaggaatg gctaaaaatg 480 tttcagagct ggagtggacc agagaaattg cttgctttag atgaactcat tgatagttgt 540 gaaccaacac aagtaaaaca tatgatgcaa gtgatagaac cccagtttca acgagacttc 600 atttcattgc tccctaaaga gttggcactc tatgtgcttt cattcctgga acccaaagac 660 ctgctacaag cagctcagac atgtcgctac tggagaattt tggctgaaga caaccttctc 720 tggagagaga aatgcaaaga agaggggatt gatgaaccat tgcacatcaa gagaagaaaa 780 gtaataaaac caggtttcat acacagtcca tggaaaagtg catacatcag acagcacaga 840 attgatacta actggaggcg aggagaactc aaatctccta aggtgctgaa aggacatgat 900 gatcatgtga tcacatgctt acagttttgt ggtaaccgaa tagttagtgg ttctgatgac 960

aacactttaa aagtttggtc agcagtcaca ggcaaatgtc tgagaacatt agtgggacat 1020 acaggtggag tatggtcatc acaaatgaga gacaacatca tcattagtgg atctacagat 1080 cggacactca aagtgtggaa tgcagagact ggagaatgta tacacacctt atatgggcat 1140 acttccactg tgcgttgtat gcatcttcat gaaaaaagag ttgttagcgg ttctcgagat 1200 qccactctta qqqtttqqqa tattqaqaca qqccaqtqtt tacatqtttt qatqqqtcat 1260 gttgcagcag tccgctgtgt tcaatatgat ggcaggaggg ttgttagtgg agcatatgat 1320 tttatggtaa aggtgtggga tccagagact gaaacctgtc tacacacgtt gcaggggcat 1380 actaatagag totattoatt acagtttgat ggtatocatg tggtgagtgg atotottgat 1440 acatcaatcc gtgtttggga tgtggagaca gggaattgca ttcacacgtt aacagggcac 1500 cagtcgttaa caagtggaat ggaactcaaa gacaatattc ttgtctctgg gaatgcagat 1560 tctacagtta aaatctggga tatcaaaaca ggacagtgtt tacaaacatt gcaaggtccc 1620 aacaagcatc agagtgctgt gacctgttta cagttcaaca agaactttgt aattaccagc 1680 tcagatgatg gaactgtaaa actatgggac ttgaaaacgg gtgaatttat tcgaaaccta 1740 gtcacattgg agagtggggg gagtggggga gttgtgtggc ggatcagagc ctcaaacaca 1800 aagctggtgt gtgcagttgg gagtcggaat gggactgaag aaaccaagct gctggtgctg 1860 gactttgatg tggacatgaa ggaattctgc agatatccag cacagtggcg gccgctcgag 1920 tctagagggc ccttcgaaca aaaactcatc tcagaagagg atctgaatat gcataccggt 1980 2001 catcatcacc atcaccattg a

72

<210> 27

<211> 666

<212> PRT

<213> Artificial Sequence

20

<220>

<223> Description of Artificial Sequence: MYCHIS tagged homo sapiens

<400> 27

Met Cys Val Pro Arg Ser Gly Leu Ile Leu Ser Cys Ile Cys Leu Tyr

1 5 10 15

Cys Gly Val Leu Leu Pro Val Leu Leu Pro Asn Leu Pro Phe Leu Thr

25

D

Cys Leu Ser Met Ser Thr Leu Glu Ser Val Thr Tyr Leu Pro Glu Lys 35 40 45

Gly Leu Tyr Cys Gln Arg Leu Pro Ser Ser Arg Thr His Gly Gly Thr
50 55 60

Glu Ser Leu Lys Gly Lys Asn Thr Glu Asn Met Gly Phe Tyr Gly Thr
65 70 75 80

Leu Lys Met Ile Phe Tyr Lys Met Lys Arg Lys Leu Asp His Gly Ser

85 90 95

Glu Val Arg Ser Phe Ser Leu Gly Lys Lys Pro Cys Lys Val Ser Glu 100 105 110

Tyr Thr Ser Thr Thr Gly Leu Val Pro Cys Ser Ala Thr Pro Thr Thr

115 120 125

Phe Gly Asp Leu Arg Ala Ala Asn Gly Gln Gly Gln Arg Arg Arg
130 135 140

Ile Thr Ser Val Gln Pro Pro Thr Gly Leu Gln Glu Trp Leu Lys Met
145 150 155 160

Phe Gln Ser Trp Ser Gly Pro Glu Lys Leu Leu Ala Leu Asp Glu Leu
165 170 175

Ile Asp Ser Cys Glu Pro Thr Gln Val Lys His Met Met Gln Val Ile 180 185 190

Glu Pro Gln Phe Gln Arg Asp Phe Ile Ser Leu Leu Pro Lys Glu Leu
195 200 205

Ala Leu Tyr Val Leu Ser Phe Leu Glu Pro Lys Asp Leu Leu Gln Ala 210 215 220

Ala Gln Thr Cys Arg Tyr Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu 225 230 235 240

Trp Arg Glu Lys Cys Lys Glu Glu Gly Ile Asp Glu Pro Leu His Ile
245 250 255

Lys Arg Arg Lys Val Ile Lys Pro Gly Phe Ile His Ser Pro Trp Lys
260 265 270

Ser Ala Tyr Ile Arg Gln His Arg Ile Asp Thr Asn Trp Arg Arg Gly
275 280 285

Glu Leu Lys Ser Pro Lys Val Leu Lys Gly His Asp Asp His Val Ile 290 295 300

Thr Cys Leu Gln Phe Cys Gly Asn Arg Ile Val Ser Gly Ser Asp Asp 305 310 315 320

Asn Thr Leu Lys Val Trp Ser Ala Val Thr Gly Lys Cys Leu Arg Thr 325 330 335

Leu Val Gly His Thr Gly Gly Val Trp Ser Ser Gln Met Arg Asp Asn 340 345 350

Ile Ile Ile Ser Gly Ser Thr Asp Arg Thr Leu Lys Val Trp Asn Ala
355 360 365

Glu Thr Gly Glu Cys Ile His Thr Leu Tyr Gly His Thr Ser Thr Val 370 375 380

Arg Cys Met His Leu His Glu Lys Arg Val Val Ser Gly Ser Arg Asp

385 390 395 400

Ala Thr Leu Arg Val Trp Asp Ile Glu Thr Gly Gln Cys Leu His Val
405 410 415

Leu Met Gly His Val Ala Ala Val Arg Cys Val Gln Tyr Asp Gly Arg
420 425 430

Arg Val Val Ser Gly Ala Tyr Asp Phe Met Val Lys Val Trp Asp Pro 435 440 445

Glu Thr Glu Thr Cys Leu His Thr Leu Gln Gly His Thr Asn Arg Val 450 455 460

Tyr Ser Leu Gln Phe Asp Gly Ile His Val Val Ser Gly Ser Leu Asp
465 470 475 480

Thr Ser Ile Arg Val Trp Asp Val Glu Thr Gly Asn Cys Ile His Thr
485 490 495

Leu Thr Gly His Gln Ser Leu Thr Ser Gly Met Glu Leu Lys Asp Asn 500 505 510

Ile Leu Val Ser Gly Asn Ala Asp Ser Thr Val Lys Ile Trp Asp Ile
515 520 525

Lys Thr Gly Gln Cys Leu Gln Thr Leu Gln Gly Pro Asn Lys His Gln 530 535 540

Ser Ala Val Thr Cys Leu Gln Phe Asn Lys Asn Phe Val Ile Thr Ser 545 550 555 560

Ser Asp Asp Gly Thr Val Lys Leu Trp Asp Leu Lys Thr Gly Glu Phe
565 570 575

Ile Arg Asn Leu Val Thr Leu Glu Ser Gly Gly Ser Gly Gly Val Val
580 585 590

Trp Arg Ile Arg Ala Ser Asn Thr Lys Leu Val Cys Ala Val Gly Ser
595 600 605

Arg Asn Gly Thr Glu Glu Thr Lys Leu Leu Val Leu Asp Phe Asp Val
610 615 620

Asp Met Lys Glu Phe Cys Arg Tyr Pro Ala Gln Trp Arg Pro Leu Glu 625 630 635 640

Ser Arg Gly Pro Phe Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn 645 650 655

Met His Thr Gly His His His His His

660 665

<210> 28

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide primer

<400> 28

tcacttcatgtccacatcaaagtcc

25

<210> 29

<211> 27

<212>	DNA		
<213>	Artificial Sequence		
<220>			
<223>	Description of Artificial	Sequence:	
	Oligonucleotide primer		
<400>	29		
ggtaat	tacaaagttcttgttgaactg	2	7
<210>	3.0		
<211>			
<212>			
	Artificial Sequence		
12137			
<220>			
	Description of Artificial	Seguence:	
	Oligonucleotide primer	2042000	
	origonacrescrae primer		
<400>	30		
	aacgtgtgtagacagg	2	2
<210>	31		
<211>	24		
<212>	DNA		
<213>	Artificial Sequence		
<220>			
<223>	Description of Artificial	Sequence:	
	Oligonucleotide primer		
<400>	31		
ccagto	tctgcattccacactttg	2	4

<210> 32

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide primer

DZ

<400> 32

ctcagacaggtcaggacatttgg

```
<211> 25
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primer
<400> 28
                                                                       25
tcacttcatgtccacatcaaagtcc
<sup>2</sup>210> 29
<211> 27
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primer
<400> 29
                                                                       27
{\tt ggtaattacaaagttcttgttgaactg}
<210> 30
<211> 22
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primer
<400> 30.
```

22 ccctgcaacgtgtgtagacagg <210> 31 <211> 24 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: Oligonucleotide primer <400> 31 ccagtctctgcattccacactttg 24 <210> 32 <211> 23 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: Oligonucleotide primer <400> 32 23 ctcagacaggtcaggacatttgg